

THE UNITED STATES PATENT AND TRADEMARK OFFICE

In the Application of:

JAMES K. PRESNAIL ET AL.

APPLICATION NO.: 09/829.481

FILED: APRIL 10, 2001

FOR: ARTHROPOD DEFENSINS

CASE NO.: BB1441 US NA

GROUP ART UNIT: 1638

EXAMINER: A. KUBELIK

AMENDMENT AND RESPONSE TO RESTRICTION REQUIREMENT

Assistant Commissioner for Patents Washington, DC 20231

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PATENT

Sir:

This is an Amendment and Response to the Restriction Requirement in the Office Action dated May 3, 2002. A Petition for Extension of Time for three (3) months up to and including September 3, 2002 is being filed simultaneously herewith. Please enter the following:

IN THE SPECIFICATION:

Please amend the specification as follows (a marked-up version showing changes made is attached hereto):

paragraph at page 9, lines 8-30

A "substantial portion" of an amino acid or nucleotide sequence comprises an amino acid or a nucleotide sequence that is sufficient to afford putative identification of the protein or gene that the amino acid or nucleotide sequence comprises. Amino acid and nucleotide sequences can be evaluated either manually by one skilled in the art, or by using computer-based sequence comparison and identification tools that employ algorithms such as BLAST (Basic Local Alignment Search Tool; Altschul et al. (1993) *J. Mol. Biol. 215*:403-410). In general, a sequence of ten or more contiguous amino acids or thirty or more contiguous nucleotides is necessary in order to putatively identify a polypeptide or nucleic acid sequence as homologous to a known protein or gene. Moreover, with respect to nucleotide sequences, genespecific oligonucleotide probes comprising 30 or more contiguous nucleotides may be used in sequence-dependent methods of gene identification (e.g., Southern hybridization) and isolation (e.g., *in situ* hybridization of bacterial colonies or bacteriophage plaques). In addition, short oligonucleotides of 12 or more nucleotides may be used as amplification primers in PCR in order to obtain a particular nucleic